

9598-066

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|   |                  |
|---|------------------|
| ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC<br>ATGTGCTTT TAAATTGGCC TCCGTGACCC GCCCACTTGG TGTAAGGAAA GAACCGGCCA<br>AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC<br>TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC<br>Met Ala Thr Ser Trp Gly Ala Val Phe | 60<br>120<br>231 |
| 1 5   |                  |
| ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG<br>Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln<br>10 15 20 25   | 279              |
| CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT<br>Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn<br>30 35 40  | 327              |
| GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT<br>Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr<br>45 50 55  | 375              |
| GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG<br>Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln<br>60 65 70  | 423              |
| CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT<br>Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu<br>75 80 85  | 471              |
| TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG<br>Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu<br>90 95 100 105   | 519              |
| CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG<br>Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg<br>110 115 120   | 567              |
| ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG<br>Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu<br>125 130 135   | 615              |
| CAG AAA GCC CAG GCT CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT<br>Gln Lys Ala Gln Ala Leu Leu Glu Val Glu Glu Ile Phe Lys Asn<br>140 145 150   | 663              |
| TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC<br>Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser<br>155 160 165   | 711              |
| TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG<br>Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln<br>170 175 180 185   | 759              |
| CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT<br>Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly<br>190 195 200   | 807              |
| GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA<br>Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu<br>205 210 215   | 855              |
| CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT<br>Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr<br>220 225 230   | 903              |

Fig. 1

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|   |      |
|---|------|
| TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA<br>Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala<br>235 240 245     | 951  |
| AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT<br>Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His<br>250 255 260 265 | 999  |
| ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC<br>Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile<br>270 275 280     | 1047 |
| TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG<br>Phe Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met<br>285 290 295         | 1095 |
| GCC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA<br>Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys<br>300 305 310     | 1143 |
| CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT<br>Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser<br>315 320 325     | 1191 |
| TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG<br>Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys<br>330 335 340 345 | 1239 |
| GCC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG<br>Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val<br>350 355 360     | 1287 |
| TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG<br>Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met<br>365 370 375     | 1335 |
| GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC<br>Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala<br>380 385 390     | 1383 |
| GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC<br>Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp<br>395 400 405     | 1431 |
| TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT<br>Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His<br>410 415 420 425     | 1479 |
| CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA<br>His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro<br>430 435 440     | 1527 |
| GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT<br>Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser<br>445 450 455     | 1575 |
| GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTT<br>Gly Lys Ala Trp Pro Glu Thr Arg<br>460 465   | 1629 |

Fig. 1 (cont'd.)

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|                       |                       |            |            |      |
|-----------------------|-----------------------|------------|------------|------|
| TAGATGAGTC TTGCTCTTGA | GCCTAGTGAT TTGGGCTTCA | ATGATTTGCA | CATCTAATGT | 1689 |
| GAATAGCTCC TAACCACTTG | GTGGGTGCAT GGCTGGCACC | AGACTGTAAA | TCTTTGGGA  | 1749 |
| TTCTTTGTAC AGAGTCCTGC | AAAGGAAAAAA           | AGAGAAAAGG | TTTGGAACTC | 1809 |
| TGCGAGTTCA GAGACAGGTC | CCTGGGACC AAAGAACAAAT | CTCGTTTCAA | CCCTTGATG  | 1869 |
| CCTCATTGCT TTGAATGGAT | TCATTTTGC TTATAAGCTG  | ATTTACTGAA | ATCCCATAAC | 1929 |
| CCATCAATGC TGTAAATTTC | TTTCTTCCTA CCCTTATTAC | ATTCCCTACC | CTAAAAGCCT | 1989 |
| GGGGGAAATA CCTGGTTTG  | CTTCCCATCT ATAATTGAGA | AAGAGGGGGG | AAAAGATACT | 2049 |
| GTATTAGAAT TTGTGTGATC | CTGTGGCACA ATAGATCAAC | CAACCCATT  | AAAGCTAAA  | 2109 |
| AAAAAAAAAA            |                       |            |            | 2119 |

FIG. 1 (cont.d.)

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peaNTPase 1 ---KELLKIKRITPFLYSWPAITSQYQCNEDLTSRVTFKQDEBISGSYAVVFDAGSTGSR  
potapyrase 1 SRLNQNSHPPFIIILAFLVLVPLSLLSKVNNAQDPRGRHLSENGE..HVALFDAGSTGSR  
mNTPase 1 SATSGWATPFMIDTACCGSTVFPYRQOTWPEGYPSNSMCPTNVSGAATGCTEDAGSTGSR  
yGDPase 1 KTPKJIGIYVYNDPFGMLDGEKTEONVPELADAVKSQTSGTSEKHNIVVADAGSTGSR

peaNTPase 57 LHVYLPENONQDLHLIGKGVEYMAATPCOAKSELIPILLEQAEDVVPPDLOP  
potapyrase 59 VHVYLPFDEKELLPIGNNIBYFVATEPCPLSSYAMDPKAANSLMPLEGAEGVVVPQILOS  
mNTPase 61 LHVYLPFVOKTAGOLPFLEGEBIPPDAYAKPCLSAVVIOPKGCAZLYQELLEVANDSIPSHWE  
yGDPase 61 VHIVLPFDVCTS...BPTLLEBKDMTEPGLSSEOTDSDVGAAANSLMPLIKVAIYVPKKARS

peaNTPase 117 CTPVPLGATAGLRLINGDASEKILQSVRDMLCNRSTS..NVCQDAAVSIMDGQEGSYLWVT  
potapyrase 119 CTPVPLGATAGLRLKGDAAEKILQAVRNWVKNQSTF..HSKQDMVILDGTOEGSYMWAN  
mNTPase 121 CTPVPLGATAGLRLPIKQAKALQVLEBEPCHN..SPL..LVPDGSVSIMDGSYECKLAHVT  
yGDPase 119 CTPVAKATAKGRLLGDAKSSKILSAVRDHEKDYBPPVMSGDOVSINGCDMECVIAWPT

peaNTPase 176 VNVIALGNLCKEYVW..TVGVIDLGGGSVQMHAYAVSKKATAKNAPKWADGDPYKKVYVKG  
potapyrase 178 INVYLGLGKGDYK..PATIDLGGSVQMHAYAISNEQFARAPQNEDG..PPVVOOKBLMS  
mNTPase 179 VNVILTCQHGGOE..TVGTIDLGGSVQMHAYAISNEQFARAPQNEDG..PPVVOOKBLMS  
yGDPase 179 TNVLLGNGCANOPKLPKAV..BLGGGSTONTKEP..TFFPINEKIVDGKHKX..DVKPQD

peaNTPase 234 ITPHLYVHVSYLEFCRASRAEILK..  
potapyrase 235 KAPLIVHVSYLIICQLGRABIFKA..  
mNTPase 232 STEKLIVHSYLGFGGLRARLATLG..  
yGDPase 234 EKVTLSKEDFTIDFIGPDEPSGAQCRPLDIEIUNKPAACQQSPPCGECVHQPSLVTPK

peaNTPase 276 TVSGEPEKATAYTSGH..N..N..X..Q..N..T..I..K..L..K..K..P..C..P..Q..N..T..F..C..G..L..W..N..C..G..G..G..  
potapyrase 277 SVOGYPMKVRDPRKGCS...SNKRCRRLTRHALKINJACM..PCTENCVNNNGGGD..  
mNTPase 270 KCEPFRNLEAEWIFPGCV..KTYOGHORGEOMGFKPCYAKYSLRVVCGDRHQPEEVN..  
yGDPase 294 EKVTLSEKEQFTIDFIGPDEPSGAQCRPLDIEIUNKPAACQQSPPCGECVHQPSLVTPK

peaNTPase 328 GOKNGCASSCHYILPEDTGKVDKATDPHMDPPIPDKK  
potapyrase 329 GOKNGCASSCHYILPEDTGKVDKATDPHMDPPIPDKK  
mNTPase 322 GSA..TVAFPSYMYDR..ADTHEDYDE..KGGYLVKVBDFPESKAREVGH..HGSFSGSP..  
yGDPase 354 ESNDEWIFSYFDRQRPLGMPLEFNLHEDNLARLIVKGEEETHVVGCHIAC..DDEL

peaNTPase 388 HIGASVYCMDDLIYVLLVDCFCPLPLOIITPCKIEVYQIAVVAAPLGNAYEAISALPR  
potapyrase 389 NM..PYLCMDLIYVLLVDCFCPLPLOIITPCKIEVYQIAVVAAPLGNAYEAISALPR  
mNTPase 374 ...EUCMDIITYITALIHDCLGFAERPLTAKESQBRDWIGLQQGILSPDVSGKHQLR  
yGDPase 411 ESDSHFCMDDLIYVLLVDCFCPLPLOIITPCKIEVYQIAVVAAPLGNAYEAISALPR

peaNTPase 446 PERGKMFV...  
potapyrase 448 KIRPAGH...  
mNTPase 430 PSSTSGACISEPVPFSQEGVDSETPSDLSCKAMPETR...  
yGDPase 467 WCKEQSGA...

F16. 2

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ACR I

**CD39**  
**ratCD39**  
**CD39L1**  
**chickATPase**  
**peaATPase**  
**potERCP1**  
**yGDA1**  
**ANTPase**  
**hCD39L2**  
**celegans**  
**w15K9**

1. ENGINERUNNING  
2. ENGINEFALLING  
3. ENGINEFALLING  
4. ENGINERUNNING  
5. ENGINERUNNING  
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19. ENGINERUNNING  
20. ENGINERUNNING

ALL INFORMATION CONTAINED  
HEREIN IS UNCLASSIFIED  
DATE 11/19/07 BY SP2 KIRKMAN

ACR II

CD39  
 ratCD39  
 CD39L1  
 chickATPase  
 peaATPase  
 potRROPI  
 yGDA1  
 hNTPase  
 hCD39L2  
 calegans

47 VOVENIX MTDCHBRRDMM 48 CHORIOT 49  
47 HOGGIE BLAIC HETTRR 48 SPOH 50  
47 GEMSHAW SHVCGHOM 49 CHP YMMDA  
47 GEMSHAW SHVCGHOM 50 DPHY  
46 BIRPOAM EBLK 51 DLOPDR  
46 BIRPOAM EBLK 52 KLOPDR  
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45 BIRPOAM EBLK 98 KLOPDR  
45 BIRPOAM EBLK 99 KLOPDR  
45 BIRPOAM EBLK 100 KLOPDR

ACB III

**CD39**  
ratCD39  
**CD39L1**  
chickATPase  
yeaATPase  
potatoY1  
yGDA1  
MTPase  
**bCD39L2**  
*c.elegans*  
-21ED

ACB IV

FIG. 3

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|   |            |            |            |            |     |
|---|------------|------------|------------|------------|-----|
| GTGGGGTCTGATCCCGCGGG  | TGGAGGCCGG | GGTGGCGCCG | GCCGGGGCGG | GGGAGCCAA  | 60  |
| AAGACCGGCTGCCGCCTGCT  | CCCCGGAAAA | GGGCACTCGT | CTCCGTGGGT | GTGGCGGAGC | 120 |
| GCGCGGTGCA  | TGGAATGGC  | TATGTGAATG | AAAAAAGGTA | TCCGTTATGA | 180 |
| AAAACGAGCT  | ACATTTTCAG | GCAGCCGCAG | CACGGTCCTT | GGCAAACAAG | 237 |
|   |            |            |            | G ATG AGA  |     |
|   |            |            |            | Met Arg    |     |
|   |            |            |            | 1          |     |
| AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC |            |            |            |            | 285 |
| Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro |            |            |            |            |     |
| 5   | 10         | 15         |            |            |     |
| CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG |            |            |            |            | 333 |
| Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp |            |            |            |            |     |
| 20  | 25         | 30         |            |            |     |
| CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC |            |            |            |            | 381 |
| His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala |            |            |            |            |     |
| 35  | 40         | 45         | 50         |            |     |
| CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT |            |            |            |            | 429 |
| Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala |            |            |            |            |     |
| 55  | 60         | 65         |            |            |     |
| GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC |            |            |            |            | 477 |
| Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser |            |            |            |            |     |
| 70  | 75         | 80         |            |            |     |
| ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA |            |            |            |            | 525 |
| Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu |            |            |            |            |     |
| 85  | 90         | 95         |            |            |     |
| ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT |            |            |            |            | 573 |
| Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu |            |            |            |            |     |
| 100   | 105        | 110        |            |            |     |
| TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA |            |            |            |            | 621 |
| Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu |            |            |            |            |     |
| 115   | 120        | 125        | 130        |            |     |
| CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC |            |            |            |            | 669 |
| Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala |            |            |            |            |     |
| 135   | 140        | 145        |            |            |     |
| ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA |            |            |            |            | 717 |
| Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly |            |            |            |            |     |
| 150   | 155        | 160        |            |            |     |
| GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA |            |            |            |            | 765 |
| Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala |            |            |            |            |     |
| 165   | 170        | 175        |            |            |     |
| TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA |            |            |            |            | 813 |
| Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr |            |            |            |            |     |
| 180   | 185        | 190        |            |            |     |
| GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC |            |            |            |            | 861 |
| Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser |            |            |            |            |     |
| 195   | 200        | 205        | 210        |            |     |
| TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA |            |            |            |            | 909 |
| Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly |            |            |            |            |     |
| 215   | 220        | 225        |            |            |     |

FIG. 4

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|  |      |
|--|------|
| GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG<br>Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln<br>230 235 240  | 957  |
| GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC<br>Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr<br>245 250 255  | 1005 |
| TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA<br>Tyr Lys Leu Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala<br>260 265 270  | 1053 |
| CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA<br>Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly<br>275 280 285 290  | 1101 |
| AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG<br>Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp<br>295 300 305  | 1149 |
| GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA<br>Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala<br>310 315 320  | 1197 |
| AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC<br>Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn<br>325 330 335  | 1245 |
| AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC<br>Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe<br>340 345 350  | 1293 |
| TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG<br>Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu<br>355 360 365 370  | 1341 |
| AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC<br>Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr<br>375 380 385  | 1389 |
| GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC<br>Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys<br>390 395 400  | 1437 |
| ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC<br>Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro<br>405 410 415  | 1485 |
| AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC<br>Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr<br>420 425 430  | 1533 |
| AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA<br>Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg<br>435 440 445 450  | 1581 |
| CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT<br>Gln Lys Ser Pro Ala Ser<br>455  | 1637 |
| GTGTGTCCTGC ATAAACCCCTC CTGTCCTGGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA<br>GGCCGTGCTG GCACCTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCC<br>TGGCATCAGC CTCTTCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC<br>1697<br>1757<br>1817 |      |

FIG. 4 (cont'd.)

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|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| AATGCCACCT  | GTCTGCCTGG | GCTCCAAGTG  | GGCAGGACCA | GGACAGAAC  | ACAGGCACAC  | 1877 |
| ACTGAGGGGG  | CAGTGTGGCT | CCCTGCCTGT  | CCCATCCCCA | TGCCCCGTCC | GCGGGGCTGT  | 1937 |
| GGCTGCTGCT  | GTGCATGTCC | CTGCGATGGG  | AGTCTTGTCT | CCCAGCCTGT | CAGTTTCCTC  | 1997 |
| CCCAAGGGCAG | AGCTCCCCTT | CCTGCAAGAG  | TCTGGGAGGC | GGTGCAGGCT | GTCCTGGCTG  | 2057 |
| CTCTGGGGAA  | GCCGAGGGAC | AGCCATAACA  | CCCCCGGGAC | AGTAGGTCTG | GGCGGCACCA  | 2117 |
| CTGGGAACTC  | TGGACTTGAG | TGTGTTGCT   | CTTCCTTGGG | TATGAATGTG | TGAGTTCAACC | 2177 |
| CAGAGGCCCTG | CTCTCCTCAC | ACATTGTGTG  | GTTTGGGTT  | AATGATGGAG | GGAGACACCT  | 2237 |
| CTTCATAGAC  | GGCAGGTGCC | CACCTTCAG   | GGAGTCTCCC | AGCATGGGCG | GATGCCGGGC  | 2297 |
| ATGAGCTGCT  | GTAAACTATT | TGTGGCTGTG  | CTGCTTGAGT | GACGTCTCTG | TCGTGTGGGT  | 2357 |
| GCCAAGTGCT  | TGTGTAGAAA | CTGTGTTCTG  | AGCCCCCTTT | TCTGGACACC | AACTGTGTCC  | 2417 |
| TGTGAATGTA  | TCGCTACTGT | GAGCTTTCC   | CGCCTAGCCA | GGGCCATGTC | TTAGGTGCAG  | 2477 |
| CTGTGCCACG  | GGTCAGCTGA | GCCACAGTCC  | CAGAACCAAG | CTCTCGGTGT | CTCGGGCCAC  | 2537 |
| CATCCGCCCA  | CCTCGGGCTG | ACCCCCACCTC | CTCCATGGAC | AGTGTGAGCC | CCGGGGCCGTG | 2597 |
| CATCCTGCTC  | AGTGTGGCGT | CAGTGTGAGG  | GCTGAGCCCC | TTGAGCTGCT | TCAGTGAATG  | 2657 |
| TACAGTGCCTC | GGCACGAGCT | GAACCTCATG  | TGTTCCACTC | CCAATAAAAG | GTTGACAGGG  | 2717 |
| GCTTCTCCTT  | AAAAAAAAAA | AAAAAAAAAA  | AAAAAAAAAA | AAAAAA     |             | 2762 |

FIG. 4 (cont'd)

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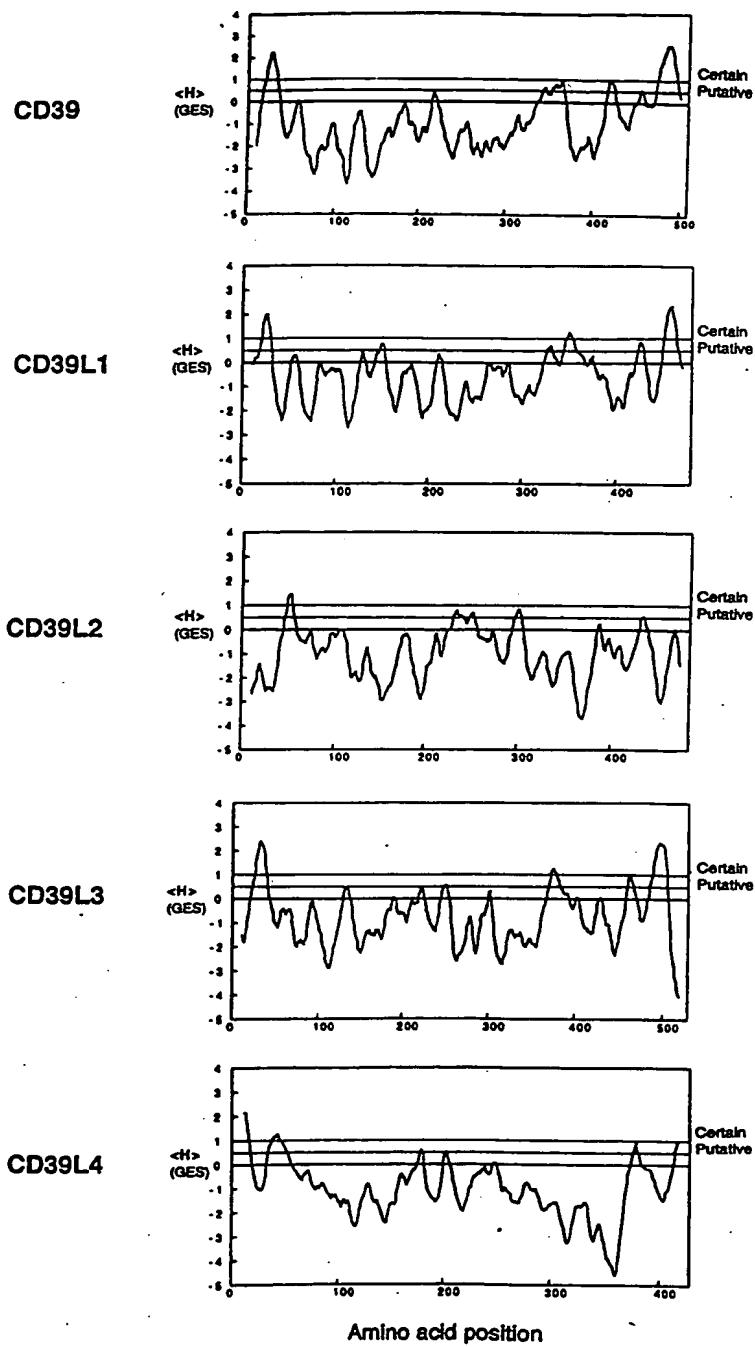


FIG. 5

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|  |           |
|--|-----------|
| ACCCACCGCGT CTGGCCGCGG GCCGCCCTCG CGGCAGCGCT AGTCGCCCTTC TCCGAATCGG<br>CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT<br>Met Phe Thr Val Leu Thr Arg Gln Pro Cys<br>1 5 10 | 60<br>112 |
| GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC<br>Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala<br>15 20 25   | 160       |
| TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC<br>Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val<br>30 35 40   | 208       |
| ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT<br>Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly<br>45 50 55   | 256       |
| ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA<br>Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln<br>60 65 70   | 304       |
| TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC<br>Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe<br>75 80 85 90  | 352       |
| AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC<br>Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro<br>95 100 105   | 400       |
| CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG<br>Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly<br>110 115 120  | 448       |
| CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC<br>Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala<br>125 130 135  | 496       |
| ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT<br>Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn<br>140 145 150  | 544       |
| GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC<br>Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp<br>155 160 165 170  | 592       |
| TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA<br>Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly<br>175 180 185  | 640       |
| TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG<br>Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu<br>190 195 200  | 688       |
| TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG<br>Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu<br>205 210 215  | 736       |
| GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG<br>Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys<br>220 225 230  | 784       |

FIG. 6

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|   |      |
|---|------|
| ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC<br>Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr<br>235 240 245 250 | 832  |
| GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG<br>Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu<br>255 260 265     | 880  |
| GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA<br>Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys<br>270 275 280     | 928  |
| AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC<br>Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe<br>285 290 295     | 976  |
| ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA<br>Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro<br>300 305 310     | 1024 |
| GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC<br>Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp<br>315 320 325 330 | 1072 |
| CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT<br>Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala<br>335 340 345     | 1120 |
| TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG<br>Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys<br>350 355 360     | 1168 |
| ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT<br>Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser<br>365 370 375     | 1216 |
| GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC<br>Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser<br>380 385 390     | 1264 |
| ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC<br>Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu<br>395 400 405 410     | 1312 |
| CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC<br>Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn<br>415 420 425     | 1360 |
| TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT<br>Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr<br>430 435 440     | 1408 |
| TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC<br>Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala<br>445 450 455     | 1456 |
| TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA<br>Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu<br>460 465 470     | 1504 |
| AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC<br>Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr<br>475 480 485 490 | 1552 |

FIG. 6 (cont'd.)

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|   |     |     |  |
|---|-----|-----|--|
| CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA<br>Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala<br>495   | 500 | 505 | 1600   |
| TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT<br>Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe<br>510   | 515 | 520 | 1648   |
| GAC CAT GCA GTG GAT TCT GAC TGAGCCTTC AAGCAGCTCC TGGAGTCCAA TGGC<br>Asp His Ala Val Asp Ser Asp<br>525  |     |     | 1703   |
| TGCTTAGAGT CAGCCTGGGT GGCACCAAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA<br>TACAACTAAC TAAAATCAAAC CACCTAGGTC ACCTGCCTCT CAAATACTGA TTTCTGCCAC<br>AGCACCTCTT GAGGCATCCC TTGGCTATTG TGTCATATT GTTCTTCAGA GACCTCACTA<br>CCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTA<br>TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATG<br>ACCTCAGGGC TCAGTTTCCA TTTCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA<br>AGCATTTCGC CAATCAGAAT CTCATTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT<br>TTCCTGTAGC AATCTCGTAA GCAGTGAAAC CCCTCAGATC AGTAGAATAT AGTATCTGGG<br>GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA<br>TCCCCAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG<br>GAATTCCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTGTC ATCATCCTCA<br>TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT<br>GCATTCAGA TTTTACTGCC TTGCTAGGC TTTGCTTAG CAAAGGGCTG ACTTTCCATT<br>GTATCATGG TGATATATT TTTGTCACCA TTCCCAAAAG TATACTTGAT GTTGTCTAG<br>AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCT<br>GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC<br>TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA<br>TTATTCATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTGA<br>AAAAAAAAA AAAA |     |     | 1763<br>1823<br>1883<br>1943<br>2003<br>2063<br>2123<br>2183<br>2243<br>2303<br>2363<br>2423<br>2483<br>2543<br>2603<br>2663<br>2723<br>2783<br>2797 |

FIG. 6 (cont'd.)

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|                     |                                 |                             |                     |             |            |     |
|---------------------|---------------------------------|-----------------------------|---------------------|-------------|------------|-----|
| GCGCGCGCGT          | TTTCCTTGT                       | CCTGGTCAAC                  | AAAGAAATGT          | GGAGTGTCTT  | GGCTGAATCC | 60  |
| TCATACAGAC          | AAGATCATTA                      | TGGTGTGTT                   | AGGTAGGACT          | TGTATCCAGA  | TGTAAGGTTG | 120 |
| AAAAAGTGAT          | ATAATAAAGG                      | AACCAAGGAG                  | AAAATTAGA           | AGGAAAGAAA  | AAATTGCCTC | 180 |
| TGCAGGTGTG          | CGAGCAGGAT                      | TGCTTCTGCA                  | ACAAAAGCT           | CCACCCCAGCC | ACATCTGGG  | 240 |
| AAAAGA ATG          | GCC ACT TCT                     | TGG GGC ACA GTC             | TTT TTC ATG         | CTG GTG GTA |            | 288 |
| Met Ala Thr Ser Trp | Gly Thr Val Phe                 | Phe Met Leu Val             | Val                 |             |            |     |
| 1                   | 5                               | 10                          |                     |             |            |     |
| TCC TGT GTT         | TGC AGC GCT                     | TCC CAC AGG AAC             | CAG CAG ACT         | TGG TTT     |            | 336 |
| Ser Cys Val         | Cys Ser Ala Val                 | Ser His Arg Asn             | Gln Gln Thr         | Trp Phe     |            |     |
| 15                  | 20                              | 25                          | 30                  |             |            |     |
| GAG GGT ATC TTC     | CTG TCT TCC ATG                 | TGC CCC ATC AAT             | GTC AGC GCC AGC     |             |            | 384 |
| Glu Gly Ile Phe     | Leu Ser Ser Met                 | Cys Pro Ile Asn             | Val Ser Ala Ser     |             |            |     |
| 35                  | 40                              | 45                          |                     |             |            |     |
| ACC TTG TAT GGA ATT | ATG TTT GAT                     | GCA GGG AGC ACT             | GGA ACT CGA ATT     |             |            | 432 |
| Thr Leu Tyr         | Gly Ile Met Phe                 | Asp Ala Gly Ser             | Thr Gly Thr Arg Ile |             |            |     |
| 50                  | 55                              | 60                          |                     |             |            |     |
| CAT GTT TAC ACC TTT | GTG CAG AAA ATG                 | CCA GGA CAG                 | CTT CCA ATT CTA     |             |            | 480 |
| His Val Tyr Thr     | Phe Val Gln Lys                 | Met Pro Gly Gln             | Leu Pro Ile Leu     |             |            |     |
| 65                  | 70                              | 75                          |                     |             |            |     |
| GAA GGG GAA GTT TTT | GAT TCT GTG AAG                 | CCA GGA CTT TCT             | GCT TTT GTA         |             |            | 528 |
| Glu Gly Glu Val     | Phe Asp Ser Val Lys             | Pro Gly Leu                 | Ser Ala Phe Val     |             |            |     |
| 80                  | 85                              | 90                          |                     |             |            |     |
| GAT CAA CCT AAG CAG | GGT GCT GAG ACC                 | GTT CAA GGG CTC TTA GAG GTG |                     |             |            | 576 |
| Asp Gln Pro Lys Gln | Gly Ala Glu Thr Val             | Gln Gly Leu Leu Glu Val     |                     |             |            |     |
| 95                  | 100                             | 105                         | 110                 |             |            |     |
| GCC AAA GAC TCA ATC | CCC CGA AGT CAC                 | TGG AAA AAG ACC CCA GTG GTC |                     |             |            | 624 |
| Ala Lys Asp Ser Ile | Pro Arg Ser His                 | Trp Lys Lys Thr Pro Val Val |                     |             |            |     |
| 115                 | 120                             | 125                         |                     |             |            |     |
| CTA AAG GCA ACA GCA | GGG CTA CGC TTA CTG CCA GAA CAC | AAA GCC AAG                 |                     |             |            | 672 |
| Leu Lys Ala Thr     | Ala Gly Leu Arg                 | Leu Leu Pro Glu His         | Lys Ala Lys         |             |            |     |
| 130                 | 135                             | 140                         |                     |             |            |     |
| GCT CTG CTC TTT     | GAG GTA AAG GAG                 | ATC TTC AGG AAG TCA CCT     | TTC CTG             |             |            | 720 |
| Ala Leu Leu Phe     | Glu Val Lys Glu                 | Ile Phe Arg Lys             | Ser Pro Phe Leu     |             |            |     |
| 145                 | 150                             | 155                         |                     |             |            |     |
| GTA CCA AAG GGC AGT | GTT AGC ATC ATG GAT             | GGA TCC GAC GAA GGC ATA     |                     |             |            | 768 |
| Val Pro Lys Gly Ser | Val Ser Ile Met Asp             | Gly Ser Asp Glu Gly Ile     |                     |             |            |     |
| 160                 | 165                             | 170                         |                     |             |            |     |
| TTA GCT TGG GTT ACT | GTG AAT TTT CTG ACA GGT         | CAG CTG CAT GGC CAC         |                     |             |            | 816 |
| Leu Ala Trp Val Thr | Val Asn Phe                     | Leu Thr Gly Gln Leu His     | Gly His             |             |            |     |
| 175                 | 180                             | 185                         | 190                 |             |            |     |
| AGA CAG GAG ACT GTG | GGG ACC TTG GAC                 | CTA GGG GGA GCC TCC ACC CAA |                     |             |            | 864 |
| Arg Gln Glu Thr Val | Gly Thr Leu Asp                 | Leu Gly Gly Ala Ser Thr Gln |                     |             |            |     |
| 195                 | 200                             | 205                         |                     |             |            |     |
| ATC ACG TTC CTG CCC | CAG TTT GAG AAA ACT             | CTG GAA CAA ACT CCT AGG     |                     |             |            | 912 |
| Ile Thr Phe Leu Pro | Gln Phe Glu Lys                 | Thr Leu Glu Gln             | Thr Pro Arg         |             |            |     |
| 210                 | 215                             | 220                         |                     |             |            |     |
| GGC TAC CTC ACT TCC | TTT GAG ATG TTT AAC AGC ACT     | TAT AAG CTC TAT             |                     |             |            | 960 |
| Gly Tyr Leu Thr Ser | Phe Glu Met Phe                 | Asn Ser Thr Tyr             | Lys Leu Tyr         |             |            |     |
| 225                 | 230                             | 235                         |                     |             |            |     |

FIG. 7

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|  |  |
|--|--|
| ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC<br>Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr<br>240 245 250  | 1008   |
| CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT<br>Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser<br>255 260 265 270  | 1056   |
| GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG<br>Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val<br>275 280 285  | 1104   |
| AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC<br>Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro<br>290 295 300  | 1152   |
| TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA<br>Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro<br>305 310 315  | 1200   |
| GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC<br>Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp<br>320 325 330  | 1248   |
| CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA<br>Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu<br>335 340 345 350  | 1296   |
| AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG<br>Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu<br>355 360 365  | 1344   |
| GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC<br>Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr<br>370 375 380  | 1392   |
| ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC<br>Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val<br>385 390 395  | 1440   |
| TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG<br>Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu<br>400 405 410  | 1488   |
| GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC<br>Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His<br>415 420 425  | 1539   |
| GTACTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG<br>TTCTGAACT AGTCTGGAC ATCCTGACT TGAGCCTAGA GATTTAGTT TAATTAATT<br>TACACATCTA ATGTGAAC TGCTGCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA<br>TCACAGAGAG CCCTGTGAGC CAAAAAGAT AGTTTGAA CTTAACCTTG GAGTGAGAGC<br>CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATTT CAACCCTTG AGTGCCTCAT<br>TCCACTGAAT ATTTAAATT TCCCTCTAA TGGTAAACTG ACTTATTGCA ATCCCAAGAC<br>CCATCAATAT CAGTATTTT TTCCCTCCCTA TACAGTGCCTC TGCCCCACCCCT TATCTGCACC<br>CACCTCCCC GAAAAAGAGA GAAAAAAA AAAAAAAA | 1599<br>1659<br>1719<br>1779<br>1839<br>1899<br>1959<br>1998 |

Fig. 7 (cont'd.)



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|            |    |                  |      |                 |     |                   |     |           |               |                |
|------------|----|------------------|------|-----------------|-----|-------------------|-----|-----------|---------------|----------------|
| peaGDP     | 2  | EELIKLITPHEFS-IP | I    | ESOYLGNM        | -LT | SRKIP             | HNE | EISVKA    | -FDAGSTGSR    | HVV            |
| potapyrase | 6  | SHEFTDIL         | -F   | LVLPLSLLSKHNVAD | -I  | PDRFLHLSE         | -.  | YAH       | -FDAGSTGSRVHV |                |
| CD39L2     | 61 | KWTRATAQDQAFS    | -T   | RPGCARGDGA      | -K  | SPSLNLLGHDWVY     | -I  | HFDAGSTG  | -RVHV-        |                |
| CD39L4     | 7  | TET              | -LVE | CVCSAV          | -H  | HRQQTPEFGH        | -L  | SGCF      | -EVSASTLY     | -FDAGSTG       |
| dNTPase    | 37 | KISGFCLXKXSVIL   | -L   | VLFVPGFVSEMAP   | -S  | HLRLSKYGYSKRVOYAN | -I  | MDAGSTG   | -RVHV-        |                |
| yGDPase    | 5  | DISHFEP          | -D   | EPFGYLDASK      | -E  | QYTPBLADA         | -K  | QSOTCSEEH | -YVIM         | -DAGSTGSRVHV-L |

|            |     | ACR II   |
|------------|-----|--|
| peaGDP     | 61  | EFHQNEQDLLEHISKG-EYV- K -PGCLSSYA -PEGAANSLIPLL QARDVVFDDLQPKTVE |
| potapyrase | 63  | MPEHKLCLLPIGNE-EYFMATE PGCLSSYA DPLVAAANSI PLLDGCAGVVPQD LQSESTP |
| CD39L2     | 119 | QFT - PPRITPAUTHTETFKAVKPGLSTYADDVEN IAG C RELLDVANQD PPGCETP    |
| CD39L4     | 66  | TFVONVQGQDQPILEGEVDFV -VKPGLSSA MDOPKQAE E FGLL VAKDS PPSHEWNTPV |
| dHTPase    | 96  | RFRNSFIDNKLIVLVEELFKERKPGLSSA ADPFLAAMS KLLDEAATV PPEHMSGTP      |
| yGDPase    | 65  | KEM - .HCTSEPTLILDEKFDM E PGLSSA DTDTSVGAANSLIPLL VAVM VVLLPESTP |

|            | ACR II                                | ACR III                          |
|------------|---------------------------------------|----------------------------------|
| peaGDP     | 121 RGCATAGLRLLNQDAEKILOAVRDLFVNSPFDN | PDAVSI DCTOEGGSYLVTVN            |
| potapyrase | 123 RGCATAGLRLNQDAEKILOAVRDLFVNSPFDN  | KSRDQWVTFV DCTOEGGSYLVTVN        |
| CD39L2     | 178 VLKATAGLRLLEFGKAYNLQWVNSPFDN      | ASPF EVCDDCVSIV CEDGEGVSAH T NEL |
| CD39L4     | 126 VLKATAGLRLLPKAKRDLFVNSPFDN        | KSPF EVPKCGAVSINLG DEG LANUTVNL  |
| dNTpase    | 156 VLKATAGLRLLPKAKRDLFVNSPFDN        | EV DAVEILMGTDEG WFTVNL           |
| yGDPase    | 123 M KATAGLRLLGDAKSGILSAVRDLFVNSPFDN | EGVIAARPTANV                     |

|            |     | ACR IV       |  |
|------------|-----|--------------|--|
| peaGDP     | 180 | LGNLCKEYTK   | FVGVLGGGSVPAIAAVSKKTAKNAPKVADGDLYPDKKVVVLKGIPVH  |
| potapyrase | 182 | LGSLGLRDVNS  | ITWLDLGGGSVPAIAAVSKKTAKNAPKVADGDLYPDKKVVVLKGIPVH |
| CD39L2     | 183 | TGSLKTPGGS   | AVGDLGGGSSTCIAFLPRVEGDTKASAPPGYLTAEFRPENFPTYK    |
| CD39L4     | 184 | TGCLLEGERQH  | FVGVLGGGSTCIAFLPQEEKDTKQTPRCYLTAEFRPENFPTYK      |
| dNTPase    | 214 | SGCRSLTKHQI  | DLGGGSSTCIAFLPQEEKDTKQTPRCYLTAEFRPENFPTYK        |
| yGDPase    | 183 | LGWRGANGPKLP | WVFDLGGGSSTCIVFEPFPIENFPTYKDGKHKFVKYQHLEEVK      |

|                   |     |   |                   |      |
|-------------------|-----|---|-------------------|------|
| <b>peaGDP</b>     | 238 | SYVHISYLGFCREAARRAELNLNLTPHSP.  | MPCLLIASTPHG      | Y    |
| <b>potapyrase</b> | 239 | DYVHISYLFGCAGRAELNLNLTPHSP.   | MPCLLIASTPHG      | Y    |
| <b>CD39L2</b>     | 239 | DYVHISYLFGCAGRAELNLNLTPHSP.   | MPCLLIASTPHG      | Y    |
| <b>CD39L4</b>     | 239 | DYVHISYLFGCAGRAELNLNLTPHSP.   | MPCLLIASTPHG      | Y    |
| <b>dNTPase</b>    | 237 | SYTHISYLGCFGLKRAELNLNLTPHSP.  | SPLCILGPFRPG      | S    |
| <b>yGDPase</b>    | 264 | FTVTHISYLGCFGLKRAELNLNLTPHSP.   | SACIICPRWLE       | S    |
|                   | 238 | SYVQSHSLG...GLKE...REIL...HSVLUVAL...ADCR...LIGDNTKTHOL...SVCPIE...PWTWV... | SVCPIE...PWTWV... | RATN |

|             |     |  |          |
|-------------|-----|--|----------|
| peaGDP      | 276 | TYEGGEVLRNAAVYTG . EHHFICLNTIR . ALKLNLIPCEYQNCCTFGG . WNGG .    | SGMGQKN  |
| potatoprase | 277 | YYGGVVRVAVKPKP . PHEG . SSWKRCRRLTREALKLNLIPCEYQNCCTFGG . WNGG . | SGDGOKK  |
| CD39L2      | 335 | EH . EHTEVTVAVKSC . KHE . ASLKHLLCAAR . . . . .                  | EEVKHVT  |
| CD39L4      | 282 | I . GGGVRYOYCC . QKGEGVCREP . STAE . . . . .                     | EEVGRS   |
| dNTPase     | 306 | TFCG . . . . . TAVSGAHRKSSASAOPIVDFFDADCG . . . . .              | EEVGRS   |
| ycGDPase    | 298 | LESKEPYT . DFIGCPDEPSGACPR . LTDFEHLT . AOCG . SPCCPES . . . . . | FTEVPAHA |

|            |     |  |
|------------|-----|--|
| peaGDP     | 332 | ...AGGSEFYLPEOTGNVDASTPNLILPVPVIEETKAKEARCALDFEDAKS...PFIDDKRNV...I  |
| potapyrase | 333 | ...EAEIILFYEIVLAVQV...VD...KPFSP...AQP...IOM...LAH...VAQ...C...T...N...DIKS...I...APK...T...O...P...H...I...P  |
| CD39L2     | 379 | ...FYAFSY...YD...LAACV...D...P...D...E...E...K...G...G...E...L...V...C...D...B...L...A...A...K...L...V...C...R...T...D...E...L...F...P...S...P   |
| CD39L4     | 326 | ...FYAFSY...YD...RAV...D...D...M...D...E...E...K...G...G...I...L...V...E...D...E...K...A...E...V...C...D...Y...D...E...F...T...S...C...P   |
| dNTPase    | 360 | ...A...A...P...F...S...Y...I...R...G...C...V...P...L...A...G...G...T...T...V...E...M...A...R...Q...B...C...I...A...I...P...H...D...E...C...P   |
| yGDPase    | 358 | ...I...Y...P...R...S...Y...F...D...R...I...P...Y...G...M...P...L...F...I...W...E...H...I...D...A...R...I...V...C...R...E...M...E...V...E...F...G...I...G...I...C...L...D...S...D...E...L...S...D...S |

|           |     |  |
|-----------|-----|--|
| peaGDP    | 392 | LCKMDLIVKQVLLVLDGFGLPLCKLITSGKHLIYTOAARVEAAWPLGMAVEALESSLPKFRR       |
| potaprase | 392 | LCKMDLIVKQVLLVLDGFGLPLCKLITSGKHLIYTOAARVEAAWPLGMAVEALESSLPKFRR       |
| CD39L2    | 428 | FECCKDLTVYSPVLLQG...FGCPFRSKVLT...KIDR...VET...EWALCAFLHMYDSLNL...SP |
| CD39L4    | 375 | FLCKMDLIVKQVLLVLDGFGLPLCKLITSGKHLIYTOAARVEAAWPLGMAVEALESSLPKFRR      |
| dNTPase   | 406 | FLCKMDLIVKQVLLVLDGFGLPLCKLITSGKHLIYTOAARVEAAWPLGMAVEALESSLPKFRR      |
| yGDPase   | 415 | HUC...DLIVKQVLLVLDGFGLPLCKLITSGKHLIYTOAARVEAAWPLGMAVEALESSLPKFRR     |

|         |     |      |
|---------|-----|------|
| peaGDP  | 452 | NYFV |
| dGTPase | 452 | AS*  |
| CD39L2  | 483 | AS*  |
| CD39L4  | 429 | ---- |
| dNTPase | 462 | ---- |
| yGDPase | 471 | QSM  |

FIG. 9